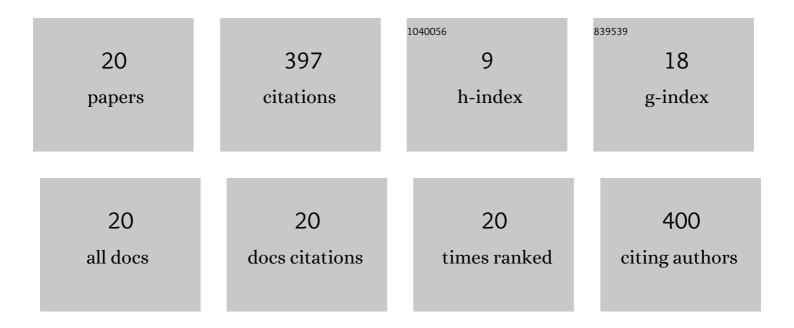
Fan Zhang

List of Publications by Year in descending order

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ΕλΝ ΖΗΛΝΟ

#	Article	IF	CITATIONS
1	Investigation of Biosurfactant-Producing Indigenous Microorganisms that Enhance Residue Oil Recovery in an Oil Reservoir After Polymer Flooding. Applied Biochemistry and Biotechnology, 2011, 163, 223-234.	2.9	68
2	Microbial diversity in long-term water-flooded oil reservoirs with different in situ temperatures in China. Scientific Reports, 2012, 2, 760.	3.3	68
3	Shifts of the indigenous microbial communities from reservoir production water in crude oil- and asphaltene-degrading microcosms. International Biodeterioration and Biodegradation, 2018, 132, 18-29.	3.9	48
4	Impact of an indigenous microbial enhanced oil recovery field trial on microbial community structure in a high pour-point oil reservoir. Applied Microbiology and Biotechnology, 2012, 95, 811-821.	3.6	46
5	Response of microbial community structure to microbial plugging in a mesothermic petroleum reservoir in China. Applied Microbiology and Biotechnology, 2010, 88, 1413-1422.	3.6	35
6	Molecular biologic techniques applied to the microbial prospecting of oil and gas in the Ban 876 gas and oil field in China. Applied Microbiology and Biotechnology, 2010, 86, 1183-1194.	3.6	30
7	Potential Microorganisms for Prevention of Paraffin Precipitation in a Hypersaline Oil Reservoir. Energy & Fuels, 2014, 28, 1191-1197.	5.1	24
8	Isolation and characterization of a crude oil degrading bacteria from formation water: comparative genomic analysis of environmental Ochrobactrum intermedium isolate versus clinical strains. Journal of Zhejiang University: Science B, 2015, 16, 865-874.	2.8	15
9	Optimization and characterization of biosurfactant produced by indigenous <i>Brevibacillus borstelensis</i> isolated from a low permeability reservoir for application in MEOR. RSC Advances, 2022, 12, 2036-2047.	3.6	11
10	Genome sequence of Brevibacillus agri strain 5-2, isolated from the formation water of petroleum reservoir. Marine Genomics, 2014, 18, 123-125.	1.1	9
11	Deposit reduction in a high pour point oil reservoir due to the activity of indigenous bacterial communities. International Biodeterioration and Biodegradation, 2016, 110, 87-98.	3.9	9
12	Genomovar assignment of Pseudomonas stutzeri populations inhabiting produced oil reservoirs. MicrobiologyOpen, 2014, 3, 446-456.	3.0	8
13	Permanent draft genome sequence of Geobacillus thermocatenulatus strain GS-1. Marine Genomics, 2014, 18, 129-131.	1.1	7
14	Dynamics of a microbial community during an effective boost MEOR trial using high-throughput sequencing. RSC Advances, 2018, 8, 690-697.	3.6	7
15	High quality genome sequence and description of Enterobacter mori strain 5–4, isolated from a mixture of formation water and crude-oil. Standards in Genomic Sciences, 2015, 10, 9.	1.5	6
16	Elucidate microbial characteristics in a full-scale treatment plant for offshore oil produced wastewater. PLoS ONE, 2021, 16, e0255836.	2.5	3
17	Draft genome sequence of Paenibacillus sp. strain A2. Standards in Genomic Sciences, 2016, 11, 9.	1.5	2
18	Tracking alterations of alkyl side chains of N ₁ species in heavy crude oil after anaerobic biodegradation with negativeâ€ion electrospray ionization coupled with highâ€field Fourier transform ion cyclotron resonance mass spectrometry. Rapid Communications in Mass Spectrometry, 2019, 33, 875-882.	1.5	1

#	Article	IF	CITATIONS
19	Anaerobic Microbial Diversity and Abundance in Xinjiang low-Temperature Water- Flooding Petroleum Reservoir. Journal of Engineering Science and Technology Review, 2017, 10, 129-135.	0.4	0
20	Microbial community diversity and potential bioremediation of drill cuttings in two oil reservoirs. Petroleum Science and Technology, 0, , 1-17.	1.5	0